



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/627,253  
Source: IFWO  
Date Processed by STIC: 1/4/04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221**

**Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/629,253

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
     Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2 ☐ Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3 ☐ Misaligned Amino  
     Numbering    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4 ☐ Non-ASCII    The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5 ☐ Variable Length    Sequence(s) 371-372 contain n's or Xaa's, representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ☐ PatentIn 2.0  
     "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7 ☐ Skipped Sequences  
     (OLD RULES)    Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
                           (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                           (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                           (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                           This sequence is intentionally skipped  
  
                           Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8 ☐ Skipped Sequences  
     (NEW RULES)    Sequence(s) \_\_\_\_\_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                           <210> sequence id number  
                           <400> sequence id number  
                           000
  
- 9 ☐ Use of n's or Xaa's  
     (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                           Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                           In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ☐ Invalid <213>  
     Response    Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11 ☐ Use of <220>    Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                           (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12 ☐ PatentIn 2.0  
     "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13 ☐ Misuse of n/Xaa    "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/627,253

DATE: 01/04/2004

TIME: 10:35:10

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\01042004\J627253.raw

3 <110> APPLICANT: Ulrich Brinkmann  
 4 Sven Hoffmeyer  
 5 Esther Mornhinweg  
 7 <120> TITLE OF INVENTION: Polymorphisms in the human gene for the multidrug  
 resistance-associated  
 8 protein 1 (MRP-1) and their use in diagnostic and therapeutic applications  
 10 <130> FILE REFERENCE: VOS-42 CON  
 12 <140> CURRENT APPLICATION NUMBER: US 10/627,253  
**C--> 13 <141> CURRENT FILING DATE: 2003-07-24**  
 15 <150> PRIOR APPLICATION NUMBER: WO 02/059142 A2  
 16 <151> PRIOR FILING DATE: 2002-01-25  
 17 <150> PRIOR APPLICATION NUMBER: EP 01 10 1651.6  
 18 <151> PRIOR FILING DATE: 2001-01-26  
 20 <160> NUMBER OF SEQ ID NOS: 405  
 22 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

5611 <210> SEQ ID NO: 371  
 5612 <211> LENGTH: (52) 51 shown  
 5613 <212> TYPE: DNA  
 5614 <213> ORGANISM: Artificial DNA Sequence  
 5616 <220> FEATURE:  
 5617 <221> NAME/KEY: source  
 5619 <223> OTHER INFORMATION: /note="Description of Artificial DNA Sequence: sequence of  
 table 3"  
 5621 <220> FEATURE:  
 5622 <223> OTHER INFORMATION: n = gcc gcc gcc or deleted OK  
 5624 <400> SEQUENCE: 371  
**E--> 5625 tccctgcgcc gccgcgcgcg ccgcgcgcgc cgcgcgcgcg naggcgtag cg**  
 5628 <210> SEQ ID NO: 372  
 5629 <211> LENGTH: (52) 51  
 5630 <212> TYPE: DNA  
 5631 <213> ORGANISM: Artificial DNA Sequence  
 5633 <220> FEATURE:  
 5634 <221> NAME/KEY: source  
 5636 <223> OTHER INFORMATION: /note="Description of Artificial DNA Sequence: sequence of  
 table 3"  
 5638 <220> FEATURE:  
 5639 <223> OTHER INFORMATION: n = ggc ggc ggc or deleted  
 5641 <400> SEQUENCE: 372  
**E--> 5642 cgctagcgct nggcggcgcc ggcggcgccg gcggcgccg gcggcgccg ga**  
 group of 9

Does Not Comply  
Corrected Diskette Needed

pp1-2,4

variable length not permitted - see item 5 on Error  
summary sheet

(52) 51

see item 5 on Error summary sheet

(52) 51

PSI: all bases MUST be in lower-case letters

10/627,253

2

<400> 405  
cccgcgcgcc gggtg

15

??

??

(...Continued)

(Continued...)

*delete at end of file*

112

3

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/627,253

DATE: 01/04/2004  
TIME: 10:35:12

Input Set : A:\PTO.FG.txt  
Output Set: N:\CRF4\01042004\J627253.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:323; Line(s) 4858  
Seq#:325; Line(s) 4896  
Seq#:327; Line(s) 4934  
Seq#:328; Line(s) 4955  
Seq#:363; Line(s) 5501  
Seq#:364; Line(s) 5518  
Seq#:367; Line(s) 5563  
Seq#:368; Line(s) 5580  
Seq#:371; Line(s) 5625  
Seq#:372; Line(s) 5642  
Seq#:375; Line(s) 5687  
Seq#:376; Line(s) 5704  
Seq#:379; Line(s) 5749  
Seq#:380; Line(s) 5766

4

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/627,253

DATE: 01/04/2004

TIME: 10:35:12

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\01042004\J627253.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:85; N Pos. 11  
Seq#:86; N Pos. 11  
Seq#:97; N Pos. 11  
Seq#:98; N Pos. 11  
Seq#:103; N Pos. 11  
Seq#:104; N Pos. 11  
Seq#:229; N Pos. 11  
Seq#:230; N Pos. 11  
Seq#:241; N Pos. 11  
Seq#:242; N Pos. 11  
Seq#:265; N Pos. 11  
Seq#:266; N Pos. 11  
Seq#:359; N Pos. 11  
Seq#:360; N Pos. 11  
Seq#:363; N Pos. 47  
Seq#:364; N Pos. 11  
Seq#:367; N Pos. 44  
Seq#:368; N Pos. 11  
Seq#:371; N Pos. 41  
Seq#:372; N Pos. 11  
Seq#:375; N Pos. 38  
Seq#:376; N Pos. 11  
Seq#:379; N Pos. 29  
Seq#:380; N Pos. 11  
Seq#:383; N Pos. 11  
Seq#:384; N Pos. 11  
Seq#:395; N Pos. 11  
Seq#:396; N Pos. 11  
Seq#:402; Xaa Pos. 6  
Seq#:404; Xaa Pos. 6

**VERIFICATION SUMMARY**

DATE: 01/04/2004

PATENT APPLICATION: US/10/627,253

TIME: 10:35:12

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\01042004\J627253.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1299 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:85  
L:1299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0  
L:1316 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:86  
L:1316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0  
L:1479 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:97  
L:1479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97 after pos.:0  
L:1496 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:98  
L:1496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:98 after pos.:0  
L:1568 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:103  
L:1568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:0  
L:1585 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:104  
L:1585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:0  
L:3451 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:229  
L:3451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:229 after pos.:0  
L:3468 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:230  
L:3468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:230 after pos.:0  
L:3631 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:241  
L:3631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:241 after pos.:0  
L:3648 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:242  
L:3648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242 after pos.:0  
L:3991 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:265  
L:3991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265 after pos.:0  
L:4008 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:266  
L:4008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:266 after pos.:0  
L:5439 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:359  
L:5439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:359 after pos.:0  
L:5456 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:360  
L:5456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:360 after pos.:0  
L:5501 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:363  
L:5501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:363 after pos.:0  
L:5501 M:112 C: (48) String data converted to lower case,  
L:5518 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:364  
L:5518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:364 after pos.:0  
L:5518 M:112 C: (48) String data converted to lower case,  
L:5563 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:367  
L:5563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:367 after pos.:0  
L:5563 M:112 C: (48) String data converted to lower case,  
L:5580 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:368  
L:5580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:368 after pos.:0  
L:5580 M:112 C: (48) String data converted to lower case,  
L:5625 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:371  
L:5625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:371 after pos.:0  
L:5625 M:254 E: No. of Bases conflict, LENGTH:Input:52 Counted:51 SEQ:371 ✓  
L:5625 M:112 C: (48) String data converted to lower case,  
L:5625 M:252 E: No. of Seq. differs, <211> LENGTH:Input:52 Found:51 SEQ:371  
L:5642 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:372  
L:5642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:372 after pos.:0

**VERIFICATION SUMMARY**PATENT APPLICATION: **US/10/627,253**

DATE: 01/04/2004

TIME: 10:35:12

Input Set : **A:\PTO.FG.txt**Output Set: **N:\CRF4\01042004\J627253.raw**

L:5642 M:254 E: No. of Bases conflict, LENGTH:Input:52 Counted:51 SEQ:372  
L:5642 M:112 C: (48) String data converted to lower case,  
L:5642 M:252 E: No. of Seq. differs, <211> LENGTH:Input:52 Found:51 SEQ:372  
L:5687 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:375  
L:5687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:375 after pos.:0  
L:5687 M:112 C: (48) String data converted to lower case,  
L:5704 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:376  
L:5704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:376 after pos.:0  
L:5704 M:112 C: (48) String data converted to lower case,  
L:5749 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:379  
L:5749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:379 after pos.:0  
L:5749 M:112 C: (48) String data converted to lower case,  
L:5766 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:380  
L:5766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:380 after pos.:0  
L:5766 M:112 C: (48) String data converted to lower case,  
L:5811 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:383  
L:5811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:383 after pos.:0  
L:5828 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:384  
L:5828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:384 after pos.:0  
L:5998 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:395  
L:5998 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:395 after pos.:0  
L:6015 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:396  
L:6015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:396 after pos.:0  
L:6109 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:402  
L:6109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:402 after pos.:0  
L:6142 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:404  
L:6142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:404 after pos.:0  
L:6164 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:6166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:405  
L:6166 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:6167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:405  
L:6167 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:6169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:405  
L:6169 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:6178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:405